

Amendments to the Specification

Please amend this application as follows:

In the title:

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~~Improvements in or relating to starch content of plants~~ Nucleic acids from cassava encoding starch branching enzyme II (SBEII) and their use

Please replace the paragraph beginning on page 9, line 30, to page 10, line 3, with the following amended paragraph:

Figure 2 shows the DNA sequence and predicted ORF of csbe2con.seq (SEQ ID NO: 39). This sequence is a consensus of 3' RACE pSJ94 and 5' RACE clones 27/9,11 and 28. The first 64 base pairs are derived from the RoRidT17 adaptor primer/dT tail followed by the SBE sequence. The one long open reading frame is shown in one letter code below the double strand DNA sequence. Also shown is the upstream ORF (MQL...LPW). (SEQ ID NO: 40)

Please replace the paragraph on page 10, line 4, beginning with "Figure 3" with the following amended paragraph:

Figure 3 shows an alignment of the 5' region of cassava SBE II csbe2con (SEQ ID NO: 41) and pSJ99 (clones 20 (SEQ ID NO: 42) and 35 (SEQ ID NO: 43)) DNA sequences. Differences from the consensus sequence are shaded.

Please replace the paragraph on page 10, line 7, beginning with "Figure 4" with the following amended paragraph:

Figure 4 shows the DNA sequence (SEQ ID NO: 28) and predicted ORF (SEQ ID NO: 29) of full length cassava SBE II tuber cDNA in pSJ107. The sequence shown is from the CSBE214 (SEQ. ID. NO. 15) to the CSBE218 (SEQ. ID. NO. 19) oligonucleotide. The DNA sequence is sequence ID No. 28 in the attached sequence listing; the amino acid sequence is Seq ID No. 29.

Please replace the paragraph on page 10, line 11, beginning with “Figure 5” with the following amended paragraph:

Figure 5 shows an alignment of 3' region of cassava SBE II pSJ116 (SEQ ID NO: 44) and 125+94 DNA sequences (SEQ ID NO: 45). The top line is the 125 + 94 sequence and the bottom SJ116 sequence.

Please replace the paragraph on page 10, line 15, beginning with “Figure 6” with the following amended paragraph:

Figure 6 shows an alignment of carboxy terminal region of pSJ116 (SEQ ID NO: 46) and 125+94 protein sequences (SEQ ID NO: 47). The top sequence is from 125+94 and the bottom from pSJ116. Identical amino acid residues are shown with the same letter, conserved changes with a colon and neutral changes with a period.

Please replace the paragraph on page 11, line 2, beginning with “Figure 8” with the following amended paragraph:

Figure 8 is an alignment of SBE II proteins. Protein sequences are indicated in one letter code. The top line represents the consensus sequence, below which is shown the consensus ruler and the individual SBE II sequences (SEQ ID Nos: 54-59). Residues matching the consensus are shaded. Dashes represent gaps introduced to optimise alignment. Sequence identities are shown at the right of the figure and are as Figure 7, except that SJ107.pro is cassava SBE II (SEQ ID NO: 29).

Please replace the paragraph on page 11, line 8, beginning with “Figure 9” with the following amended paragraph:

Figure 9 shows the DNA sequence (SEQ ID NO: 48) and predicted ORF (SEQ ID NO: 49) of a

cassava SBE II cDNA isolated by 3' RACE (plasmid pSJ 101).

Please replace the paragraph on page 11, line 10, beginning with "Figure 10" with the following amended paragraph:

Figure 10 shows the consensus DNA sequence (SEQ ID NO: 50) and predicted ORF (SEQ ID NO: 51) of a second cassava SBE II cDNA isolated by 3' and 5' RACE (sequence designated 125+94 is from plasmid pSJ125 and pSJ94, spliced at the CSBE217, SEQ. ID. NO. 18, oligo sequence).

Please replace the paragraph on page 12, line 5, beginning with "Figure 13" with the following amended paragraph:

Figure 13 shows the DNA sequence (SEQ ID NO: 30) and predicted ORF (SEQ ID NO: 31) of a second full length cassava SBE II tuber cDNA in pSJ146. Nucleotides 35-2760 are SBE II sequence (SEQ ID NO: 52) and the remainder are from the pT7Blue vector (SEQ ID NO: 53). The DNA sequence of Figure 13 is Seq ID No. 30, and the amino acid sequence is Seq ID No. 31, in the attached sequence listing.

Please replace the paragraph beginning on page 19, line 17 to page 20, line 8, with the following amended paragraph:

A comparison of all known SBE II protein sequences shows that the cassava SBE II gene is most closely related to the pea gene (Figure 8). The two proteins are 86.3% identical over a 686 amino acid range which extends from the triple proline "elbow" (Burton *et al.*, 1995 Plant J. 7, 3-15) to the conserved VVYA (SEQ ID NO: 36) sequence immediately preceding the C-terminal extensions (data not shown). All SBE II proteins are conserved over this range in that they are at least 80% similar to each other. Remarkably however, the sequence conservation between the pea, potato and cassava SBE II proteins also extends to the N-terminal transit peptide, especially the first 12 amino acids of the precursor protein and the region surrounding the mature terminus